SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: The University of Leicester
        (B) STREET: University Road
        (C) CITY: Leicester
        (E) COUNTRY: United Kingdom
        (F) POSTAL CODE (ZIP): LE1 7RH

    (ii) TITLE OF INVENTION: Complement Inhibitor

    (iii) NUMBER OF SEQUENCES: 14

    (iv) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4229 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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TCGAGTCAAC TGCTCCCAGA TAGATCCAAG ACATGAGACT GTCAGCAAGA ATTATTTGGC      60

TTATATTATG GACTGTTTGT GTAGCAGAAG ATTGTAAAGG TCCTCCTCCA AGAGAAAATT     120

CAGAAATTCT CTCAGGTTCG TGGTCTGAAC AACTATATTC AGAAGGCACT CAGGCAACCT     180

ACAAATGCCG CCCTGGATAC CGAACACTTG GTACTATTGT AAAAGTATGC AAGAATGGAG     240

AATGGGTACC TTCTAACCCA TCAAGGATAT GTCGGAAAAG GCCATGTGGG CATCCCGGAG     300

ACACACCCTT TGGGTCCTTT AGGCTGGCAG TTGGATCTGA ATTTGAATTT GGTGCAAAGG     360

TTGTTTATAC ATGTGATGAA GGGTACCAAC TATTAGGTGA AATTGATTAC CGTGAATGTG     420

ATGCAGATGG GTGGACCAAT GATATTCCAA TATGTGAAGT TGTGAAGTGC TTGCCAGTGA     480

CAGAACTGGA GAATGGAAGA ATTGTGAGTG GTGCAGCCGA ACCAGACCAG GAATATTATT     540

TTGGACAGGT GGTACGCTTT GAATGCAACT CCGGCTTCAA GATTGAAGGA CAGAAAGAAA     600

TGCACTGCTC ATAAAATGGC CTCTGGAGCA ATGAAAAGCC ACAGTGTGTG GAAATTTCTT     660
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GCCTGCCACC ACGAGTTGAA AATGGAGATG GTATATATCT GAAACCAGTT TACAAGGAGA      720

ATGAAAGATT CCAATATAAA TGTAAGCAAG GTTTTGTGTA CAAAGAAAGA GGGGATGCTG      780

TCTGCACGGG TTCTGGATGG AATCCTCAGC CTTCCTGTGA AGAAATGACA TGTTTGACTC      840

CATATATTCC AAATGGTATC TACACACCTC ACAGGATTAA ACACAGAATT GATGATGAAA      900

TCAGATATGA ATGTAAAAAT GGCTTCTATC CTGCAACCCG ATCACCTGTT TCAAAGTGTA      960

CAATTACTGG CTGGATCCCT GCTCCAAGAT GTAGCTTGAA ACCTTGTGAT TTTCCACAAT     1020

TCAAACATGG ACGTCTGTAT TATGAAGAAA GCCGGAGACC CTACTTCCCA GTACCTATAG     1080

GAAAGGAGTA CAGCTATAAC TGTGACAACG GGTTTACAAC GCCTTCACAG TCATACTGGG     1140

ACTACCTTCG TTGCACAGTA AATGGGTGGG AGCCTGAAGT TCCATGCCTC AGGCAATGTA     1200

TTTTCCATTA TGTGGAATAT GGAGAATCTT CATACTGGCA AGAAGATAT ATAGAGGGTC      1260

AGTCTGCAAA AGTCCAGTGT CACAGTGGCT ATAGTCTTCC AAATGGTCAA GATACATATT     1320

ATTGTACAGA GAATGGCTGG TCCCCTCCTC CCAAATGCGT CCGTATCAAG ACTTGTTCAG     1380

TATCAGATAT AGAAATTGAA AATGGGTTTT TTTCTGAATC TGATTATACA TATGCTCTAA     1440

ATAGAAAAAC ACGGTATAGA TGTAAACAGG GATATGTAAC AAATACCGGA GAAATATCAG     1500

GAATAATTAC TTGTCTTCAA GATGGATGGT CACCTCGACC CTCATGCATT AAGTCTTGTG     1560

ATATGCCTGT ATTTGAGAAT TCTATGACTA AGAATAATAA CACATGGTTT AAACTCAATG     1620

ACAAATTAGA CTATGAATGT CACATTGGAT ATGAAAATGA ATATAAACAT ACCAAAGGCT     1680

CTATAACATG TACTTATGAT GGATGGTCTA GTACACCTC CTGTTATGAA AGAGAATGCA      1740

GCATTCCCCT GTTACACCAA GACTTAGTTG TTTTTCCCAG AGAAGTAAAA TACAAAGTTG     1800

GAGATTCGTT GAGTTTCTCT TGCCGTTCAG GACACAGAGT TGGAGCAGAT TTAGTGCAAT     1860

GCTACCACTT TGGATGGTCC CCTAATTTCC CAACGTGTGA AGGCCAAGTA AAATCATGTG     1920

ACCAACCTCT TGAAATCCCG AATGGGGAAA TAAAGGGAAC AAAAAAAGTT GAATACAGCC     1980

ATGGTGACGT GGTGGAATAT GATTGCAAAC CTAGATTTCT ACTGAAGGGA CCCAATAAAA     2040

TCCAGTGTGT TGACGGGAAG TGGACAAGGT TGCCGATATG CGTTGAGTAT GAGAGAACAT     2100

GTGGAGACCT TCCTGAACTT GAGCATGGCT CTGTCAAGTT ATCTGTCCCT CCCTACCATC     2160

ATGGAGATTC AGTGGAGTTC ACTTGTACAG AAACCTTCAC AATGATTGGA CATGCAGTAG     2220

TTTTCTGCAT TAGTGGAAGG TGGACCGAGC TTCCTCAATG TGTTGCAACA GATCAACTGG     2280

AGAAGTGTAA AGCCCCGAAG TCAACTGGCA TAGATGCAAT TCATCCAAAT AAGAATGAAT     2340
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TTAATCATAA CTTTAGTGTG AGTTACAGAT GTAGACAAAA GCAGGAGTAT GAACATTCAA    2400

TCTGCATCAA TGGAAGATGG GATCCTGAAC CAAACTGTAC AAGCAAAAGA TTCTGCCCTC    2460

CTCCCCCGCA GATTCCAAAT GCCCAAGTGA TTGAAACCAC CGTGAAATAC TTGGATGGAG    2520

AAAAAGTATC TGTTCTTTGC CAAGATGGTT ACCTAACTCA GGGCCCAGAA GAAATGGTGT    2580

GTAAACATGG AAGGTGGCAG TCGTTACCAC GCTGCACGGA AAAAATTCCA TGTTCCCAGC    2640

CCCCTAAAAT TGAACATGGA TCTATTAAGT CGCCCAGGTC CTCAGAAGAG AGGAGAGATT    2700

TAATTGAGTC CAGCAGTTAT GAACACGGAA CTACATTCAG CTATTGCTGT AGAGATGGAT    2760

TCAAGATATC TGAAGAAAAT AGGGTAACCT GCAACATGGG AAAATGGAGC TCTCTGCCTC    2820

GTTGTGTTGG AATACCTTGT GGACCCCAC CTTCAATTCC TCTTGGTATT GTTTCTCATG    2880

AACTAGAAAG TTACCAATAT GGAGAGGAGG TTACATACAA TTGTTCTGAA GGCTTTGGAA    2940

TTGATGGACC AGCATTTATT AAATGTGTAG GAGGACAGTG GTCTGAACCT CCCAAATGCA    3000

TAAAAACTGA TTGTGACAAC TTGCCCACAT TTGAAATTGC CAAACCGACA GAAAAGAAAA    3060

AAAAATCATA CAGGTCAGGA GAACAAGTGA CATTCAGATG TCCACCTCCG TATCGAATGG    3120

ATGGCTCTGA CATTGTCACA TGTGTTAATA CGAAGTGGAT TGGACAGCCG GTATGCAAAG    3180

ATAATTCCTG TGTGAATCCA CCACATGTGC CAAATGCTAC TATACTAACA AGGCACAAGA    3240

CTAAATATCC ATCTGGTGAC AAAGTACGTT ATGACTGTAA TAAACCTTTT GAATTATTTG    3300

GGGAAGTGGA AGTGATGTGC CAAAACGGGA TTTGGACAGA ACCACCGAAA TGCAAAGATT    3360

CAACAGGGAA ATGTGGGCCT CCTCCACCTA TTGACAATGG AGACATCACC TCCTTGTCAT    3420

TACCAGTATA TGCACCATTA TCATCAGTTG AATATCAATG CCAGAACTAT TATCTACTTA    3480

AGGGAAATAA GATAGTAACA TGTAGAAATG GAAAGTGGTC TCAGCCACCA ACCTGCTTAC    3540

ATGCATGTGT GATACCAGAA GATATTATGG AAAAACATAA TATAGTTCTC AGATGGAGGG    3600

AAAATGCAAA GATTTATTCC CAATCAGGGG AGAATATTGA ATTCATGTGT AAACCTGGAT    3660

ATAGAAAATT CAGAGGATCA CCTCCGTTTC GTACAAAGTG CATTGAGGGT CACATCAATT    3720

ATCCCACTTG TGTATAAAAT CGCTATACAA TTATTAGTAA ACCTTATGGA TGAGAAATGC    3780

ACATGTATAT TACTAATACA GTTTGAATTT ACATTTAAAT ATTGTTTAGC TCATTTCCTC    3840

TAATAAGTAT ATAAACTTTT TTTATATGGT GGTTAATCAG TAACTTTACA GACTGTTGCC    3900

ACAAAGCAAG AACATTACAT TCAAAACTCC TAATCCAAAT ATGATATGTC CAAGGACAAA    3960

CTATGTCTAA GCAAGAAAAT AAATGTTAGT TCTTCAATGT CTGTTTTTAT TCAGGACCTT    4020
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TCAGATTTTC TTGGATACCT TTTGTTAGGT TCTGATTCAC AGTGAGTGGA AGACACACTG   4080

ACTCTGACTT CAAATTAGTA TTACTTGCAA TACATTAACA ACCAAACTAT CATAATATCA   4140

CAAATGTATA CAGCTAATTA CTGTGTCCTA CCTTTGTATC AATAAAGAAA TCTAAGAAAG   4200

TTCTTGCTTA AAAAAAAAAA AAAAAAAA   4229

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 866 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCGAGTCAAC TGCTCCCAGA TAGATCCAAG ACATGAGACT GTCAGCAAGA ATTATTTGGC   60

TTATATTATG GACTGTTTGT GTAGCAGAAG ATTGTAAAGG TCCTCCTCCA AGAGAAAATT   120

CAGAAATTCT CTCAGGTTCG TGGTCTGAAC AACTATATTC AGAAGGCACT CAGGCAACCT   180

ACAAATGCCG CCCTGGATAC CGAACACTTG GTACTATTGT AAAAGTATGC AAGAATGGAG   240

AATGGGTACC TTCTAACCCA TCAAGGATAT GTCGGAAAAG GCCATGTGGG CATCCCGGAG   300

ACACACCCTT TGGGTCCTTT AGGCTGGCAG TTGGATCTGA ATTTGAATTT GGTGCAAAGG   360

TTGTTTATAC ATGTGATGAA GGGTACCAAC TATTAGGTGA AATTGATTAC CGTGAATGTG   420

ATGCAGATGG GTGGACCAAT GATATTCCAA TATGTGAAGT TGTGAAGTGC TTGCCAGTGA   480

CAGAACTGGA GAATGGAAGA ATTGTGAGTG GTGCAGCCGA ACCAGACCAG GAATATTATT   540

TTGGACAGGT GGTACGCTTT GAATGCAACT CCGGCTTCAA GATTGAAGGA CAGAAAGAAA   600

TGCACTGCTC ATAAAATGGC CTCTGGAGCA ATGAAAAGCC ACAGTGTGTG GAAATTTCTT   660

GCCTGCCACC ACGAGTTGAA AATGGAGATG GATATAGAAA ATTCAGAGGA TCACCTCCGT   720

TTCGTACAAA GTGCATTGAG GGTCACATCA ATTATCCCAC TTGTGTATAA AATCGCTATA   780

CAATTATTAG TAAACCTTAT GGATGACACT TTGTTTAGAA ATGCACATGT ATATTACTAA   840

TACAGTTTGA ATTTACATTT GAAAAA   866

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2715 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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TCGAGTCAAC TGCTCCCAGA TAGATCCAAG ACATGAGACT GTCAGCAAGA ATTATTTGGC      60

TTATATTATG GACTGTTTGT GTAGCAGAAG ATTGTAAAGG TCCTCCTCCA AGAGAAAATT     120

CAGAAATTCT CTCAGGTTCG TGGTCTGAAC AACTATATTC AGAAGGCACT CAGGCAACCT     180

ACAAATGCCG CCCTGGATAC CGAACACTTG GTACTATTGT AAAAGTATGC AAGAATGGAG     240

AATGGGTACC TTCTAACCCA TCAAGGATAT GTCGGAAAAG GCCATGTGGG CATCCCGGAG     300

ACACACCCTT TGGGTCCTTT AGGCTGGCAG TTGGATCTGA ATTTGAATTT GGTGCAAAGG     360

TTGTTTATAC ATGTGATGAA GGGTACCAAC TATTAGGTGA AATTGATTAC CGTGAATGTG     420

ATGCAGATGG GTGGACCAAT GATATTCCAA TATGTGAAGT TGTGAAGTGC TTGCCAGTGA     480

CAGAACTGGA GAATGGAAGA ATTGTGAGTG GTGCAGCCGA ACCAGACCAG GAATATTATT     540

TTGGACAGGT GGTACGCTTT GAATGCAACT CCGGCTTCAA GATTGAAGGA CAGAAAGAAA     600

TGCACTGCTC ATAAAATGGC CTCTGGAGCA ATGAAAGCC ACAGTGTGTG TTGAAACCTT      660

GTGATTTTCC ACAATTCAAA CATGGACGTC TGTATTATGA AGAAAGCCGG AGACCCTACT     720

TCCCAGTACC TATAGGAAAG GAGTACAGCT ATAACTGTGA CAACGGGTTT ACAACGCCTT     780

CACAGTCATA CTGGGACTAC CTTCGTTGCA CAGTAAATGG GTGGGAGCCT GAAGTTCCAT     840

GCCTCAGGCA ATGTATTTTC CATTATGTGG AATATGGAGA ATCTTCATAC TGGCAAAGAA     900

GATATATAGA GGGTCAGTCT GCAAAAGTCC AGTGTCACAG TGGCTATAGT CTTCCAAATG     960

GTCAAGATAC ATATTATTGT ACAGAGAATG GCTGGTCCCC TCCTCCCAAA TGCGTCCGTA    1020

TCAAGACTTG TTCAGTATCA GATATAGAAA TTGAAAATGG GTTTTTTTCT GAATCTGATT    1080

ATACATATGC TCTAAATAGA AAAACACGGT ATAGATGTAA ACAGGGATAT GTAACAAATA    1140

CCGGAGAAAT ATCAGGAATA ATTACTTGTC TTCAAGATGG ATGGTCACCT CGACCCTCAT    1200

GCATTAAGTC TTGTGATATG CCTGTATTTG AGAATTCTAT GACTAAGAAT AATAACACAT    1260

GGTTTAAACT CAATGACAAA TTAGACTATG AATGTCACAT GGATATGAA AATGAATATA     1320

AACATACCAA AGGCTCTATA ACATGTACTT ATGATGGATG TCTAGTACA CCCTCCTGTT      1380

ATGAAAGAGA ATGCAGCATT CCCCTGTTAC ACCAAGACTT AGTTGTTTTT CCCAGAGAAG    1440

TAAAATACAA AGTTGGAGAT TCGTTGAGTT CTCTTGCCG TTCAGGACAC AGAGTTGGAG      1500

CAGATTTAGT GCAATGCTAC CACTTTGGAT GGTCCCCTAA TTTCCCAACG TGTGAAGGCC    1560

AAGTAAAATC ATGTGACCAA CCTCTTGAAA TCCCGAATGG GGAAATAAAG GGAACAAAAA    1620
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AAGTTGAATA CAGCCATGGT GACGTGGTGG AATATGATTG CAAACCTAGA TTTCTACTGA     1680

AGGGACCCAA TAAAATCCAG TGTGTTGACG GGAAGTGGAC AAGGTTGCCG ATATGCGTTG     1740

AGTATGAGAG AACATGTGGA GACCTTCCTG AACTTGAGCA TGGCTCTGTC AAGTTATCTG     1800

TCCCTCCCTA CCATCATGGA GATTCAGTGG AGTTCACTTG TACAGAAACC TTCACAATGA     1860

TTGGACATGC AGTAGTTTTC TGCATTAGTG GAAGGTGGAC CGAGCTTCCT CAATGTGTTG     1920

CAACAGATCA ACTGGAGAAG TGTAAAGCCC CGAAGTCAAC TGGCATAGAT GCAATTCATC     1980

CAAATAAGAA TGAATTTAAT CATAACTTTA GTGTGAGTTA CAGATGTAGA CAAAAGCAGG     2040

AGTATGAACA TTCAATCTGC ATCAATGGAA GATGGGATCC TGAACCAAAC TGTACAAGCA     2100

AAAGATTCTG CCCTCCTCCC CCGCAGATTC CAAATGCCCA AGTGATTGAA ACCACCGTGA     2160

AATACTTGGA TGGAGAAAAA GTATCTGTTC TTTGCCAAGA TGGTTACCTA ACTCAGGGCC     2220

CAGAAGAAAT GGTGTGTAAA CATGGAAGGT GGCAGTCGTT ACCACGCTGC ACGGAAAAAA     2280

TTCCATGTTC CCAGCCCCCT AAAATTGAAC ATGGATCTAT TAAGTCGCCC AGGTCCTCAG     2340

AAGAGAGGAG AGATTTAATT GAGTCCAGCA GTTATGAACA CGGAACTACA TTCAGCTATT     2400

GCTGTAGAGA TGGATTCAAG ATATCTGAAG AAAATAGGGT AACCTGCAAC ATGGGAAAAT     2460

GGAGCTCTCT GCCTCGTTGT GTTGGAATAC CTTGTGGACC CCCACCTTCA ATTCCTCTTG     2520

GTATTGTTTC TCATGAACTA GAAAGTTACC AATATGGAGA GGAGGTTACA TACAATTGTT     2580

CTGAAGGCTT TGGAATTGAT GGACCAGCAT TTATTAAATG TGTAGGAGGA CAGTGGTCTG     2640

AACCTCCCAA ATGCATAAAA ACTGATTGTG ACAACTTGCC CACATTTGAA ATTGCCAAAC     2700

CGACAGAAAA GAAAA                                                    2715
```

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1532 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
TCGAGTCAAC TGCTCCCAGA TAGATCCAAG ACATGAGACT GTCAGCAAGA ATTATTTGGC       60

TTATATTATG GACTGTTTGT GTAGCAGAAG ATTGTAAAGG TCCTCCTCCA AGAGAAAATT      120

CAGAAATTCT CTCAGGTTCG TGGTCTGAAC AACTATATTC AGAAGGCACT CAGGCAACCT      180

ACAAATGCCG CCCTGGATAC CGAACACTTG GTACTATTGT AAAAGTATGC AAGAATGGAG      240
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AATGGGTACC TTCTAACCCA TCAAGGATAT GTCGGAAAAG GCCATGTGGG CATCCCGGAG      300

ACACACCCTT TGGGTCCTTT AGGCTGGCAG TTGGATCTGA ATTTGAATTT GGTGCAAAGG      360

TTGTTTATAC ATGTGATGAA GGGTACCAAC TATTAGGTGA AATTGATTAC CGTTATCGAA      420

TGGATGGCTC TGACATTGTC ACATGTGTTA ATACGAAGTG GATTGGACAG CCGGTATGCA      480

AAGATAATTC CTGTGTGAAT CCACCACATG TGCCAAATGC TACTATACTA ACAAGGCACA      540

AGACTAAATA TCCATCTGGT GACAAAGTAC GTTATGACTG TAATAAACCT TTTGAATTAT      600

TTGGGGAAGT GGAAGTGATG TGCCAAAACG GGATTTGGAC AGAACCACCG AAATGCAAAG      660

ATTCAACAGG GAAATGTGGG CCTCCTCCAC CTATTGACAA TGGAGACATC ACCTCCTTGT      720

CATTACCAGT ATATGCACCA TTATCATCAG TTGAATATCA ATGCCAGAAC TATTATCTAC      780

TTAAGGGAAA TAAGATAGTA ACATGTAGAA ATGGAAAGTG GTCTCAGCCA CCAACCTGCT      840

TACATGCATG TGTGATACCA GAAGATATTA TGGAAAAACA TAATATAGTT CTCAGATGGA      900

GGGAAAATGC AAAGATTTAT TCCCAATCAG GGGAGAATAT TGAATTCATG TGTAAACCTG      960

GATATAGAAA ATTCAGAGGA TCACCTCCGT TTCGTACAAA GTGCATTGAG GGTCACATCA     1020

ATTATCCCAC TTGTGTATAA AATCGCTATA CAATTATTAG TAAACCTTAT GGATGAGAAA     1080

TGCACATGTA TATTACTAAT ACAGTTTGAA TTTACATTTA AATATTGTTT AGCTCATTTC     1140

CTCTAATAAG TATATAAACT TTTTTTATAT GGTGGTTAAT CAGTAACTTT ACAGACTGTT     1200

GCCACAAAGC AAGAACATTA CATTCAAAAC TCCTAATCCA AATATGATAT GTCCAAGGAC     1260

AAACTATGTC TAAGCAAGAA AATAAATGTT AGTTCTTCAA TGTCTGTTTT TATTCAGGAC     1320

CTTTCAGATT TTCTTGGATA CCTTTTGTTA GGTTCTGATT CACAGTGAGT GGAAGACACA     1380

CTGACTCTGA CTTCAAATTA GTATTACTTG CAATACATTA ACAACCAAAC TATCATAATA     1440

TCACAAATGT ATACAGCTAA TTACTGTGTC CTACCTTTGT ATCAATAAAG AAATCTAAGA     1500

AAGTTCTTGC TTAAAAAAAA AAAAAAAAA AA                                    1532
```

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTCAAGTAAC GTTAGAAGCT TAAGATG   27

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCGGCCGCT CAAATCTTCT GAGATATAGG AGA   33

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGCGGCCGCT CATTTAATCC TTAAAGGTGA GTA   33

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGCGGCCGCT CATACTGGAA AGTATGGTCT ACG   33

(2) INFORMATION FOR SEQ ID NO: 9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 207 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

    Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
    1   5   10   15

    Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
            20   25   30

```
Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
         35              40              45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
    50              55              60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65              70              75              80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
             85              90              95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
             100             105             110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
         115             120             125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
    130             135             140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145             150             155             160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
             165             170             175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
             180             185             190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile
    195             200             205
```

(2) INFORMATION FOR SEQ ID NO: 10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 265 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1               5               10              15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
             20              25              30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
         35              40              45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
    50              55              60
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Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65              70              75              80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
            85              90              95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
            100             105             110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
            115             120             125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
    130             135             140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145             150             155             160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
            165             170             175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
            180             185             190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
        195             200             205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
    210             215             220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225             230             235             240

Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn
            245             250             255

Gly Asp Tyr Ser Pro Leu Arg Ile Lys
            260             265
```

(2) INFORMATION FOR SEQ ID NO: 11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 329 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1               5               10              15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
        20              25              30
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Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
        35            40              45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
    50            55              60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65            70              75                      80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
                85              90                  95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
            100             105             110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
            115             120             125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
    130             135             140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145             150             155             160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
            165             170             175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
            180             185             190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
    195             200             205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
    210             215             220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225             230             235             240

Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn
            245             250             255

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
            260             265             270

Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr
    275             280             285

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
    290             295             300

Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr His Glu
305             310             315             320

Asn Met Arg Arg Pro Tyr Phe Pro Val
            325
```

(2) INFORMATION FOR SEQ ID NO: 12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTCCTCCTG GAAATGTTAG AAGCTTAAGA TG   32

(2) INFORMATION FOR SEQ ID NO: 13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCTCTAGATT ACTTGATACG GACGCATTT   29

(2) INFORMATION FOR SEQ ID NO: 14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 428 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Glu Asp Cys Lys Gly Pro Pro Pro Arg Glu Asn Ser Glu Ile Leu Ser
1   5   10   15

Gly Ser Trp Ser Glu Gln Leu Tyr Ser Glu Gly Thr Gln Ala Thr Tyr
            20   25   30

Lys Cys Arg Pro Gly Tyr Arg Thr Leu Gly Thr Ile Val Lys Val Cys
            35   40   45

Lys Asn Gly Glu Trp Val Pro Ser Asn Pro Ser Arg Ile Cys Arg Lys
50   55   60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Ser Phe Arg Leu
65   70   75   80

Ala Val Gly Ser Glu Phe Glu Phe Gly Ala Lys Val Val Tyr Thr Cys
                85   90   95

Asp Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asp Tyr Arg Glu Cys Asp

```
              100                    105                    110
Ala Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
         115                    120                    125

Leu Pro Val Thr Glu Leu Glu Asn Gly Arg Ile Val Ser Gly Ala Ala
         130                    135                    140

Glu Pro Asp Gln Glu Tyr Tyr Phe Gly Gln Val Val Arg Phe Glu Cys
145                    150                    155                    160

Asn Ser Gly Phe Lys Ile Glu Gly Gln Lys Glu Met His Cys Ser Glu
                   165                    170                    175

Asn Gly Leu Trp Ser Asn Glu Lys Pro Gln Cys Val Glu Ile Ser Cys
                   180                    185                    190

Leu Pro Pro Arg Val Glu Asn Gly Asp Gly Ile Tyr Leu Lys Pro Val
                   195                    200                    205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Lys Gln Gly Phe Val
         210                    215                    220

Tyr Lys Glu Arg Gly Asp Ala Val Cys Thr Gly Ser Gly Trp Asn Pro
225                    230                    235                    240

Gln Pro Ser Cys Glu Glu Met Thr Cys Leu Thr Pro Tyr Ile Pro Asn
                   245                    250                    255

Gly Ile Tyr Thr Pro His Arg Ile Lys His Arg Ile Asp Asp Glu Ile
                   260                    265                    270

Arg Tyr Glu Cys Lys Asn Gly Phe Tyr Pro Ala Thr Arg Ser Pro Val
         275                    280                    285

Ser Lys Cys Thr Ile Thr Gly Trp Ile Pro Ala Pro Arg Cys Ser Leu
         290                    295                    300

Lys Pro Cys Asp Phe Pro Gln Phe Lys His Gly Arg Leu Tyr Tyr Glu
305                    310                    315                    320

Glu Ser Arg Arg Pro Tyr Phe Pro Val Pro Ile Gly Lys Glu Tyr Ser
                   325                    330                    335

Tyr Tyr Cys Asp Asn Gly Phe Thr Thr Pro Ser Gln Ser Tyr Trp Asp
                   340                    345                    350

Tyr Leu Arg Cys Thr Val Asn Gly Trp Glu Pro Glu Val Pro Cys Leu
                   355                    360                    365

Arg Gln Cys Ile Phe His Tyr Val Glu Tyr Gly Glu Ser Ser Tyr Trp
         370                    375                    380

Gln Arg Arg Tyr Ile Glu Gly Gln Ser Ala Lys Val Gln Cys His Ser
385                    390                    395                    400
```

Gly Tyr Ser Leu Pro Asn Gly Gln Asp Thr Tyr Tyr Cys Thr Glu Asn
                    405   410   415

Gly Trp Ser Pro Pro Pro Lys Cys Val Arg Ile Lys
              420   425

Figure 1

```
                    10        20        30 -18    40        50        60
          tcgagtcaactgctcccagatagatccaagacATGAGACTGTCAGCAAGAATTATTTGGC        rFH4.3
          tcgagtcaactgctcccagatagatccaagacATGAGACTGTCAGCAAGAATTATTTGGC        rFH2.7
          tcgagtcaactgctcccagatagatccaagacATGAGACTGTCAGCAAGAATTATTTGGC        rFH1.8
          tcgagtcaactgctcccagatagatccaagacATGAGACTGTCAGCAAGAATTATTTGGC        rFH1.0


                                        SCR1
                    70        80       +1 90      100       110       120
          TTATATTATGGACTGTTTGTGTAGCAGAAGATTGTAAAGGTCCTCCTCCAAGAGAAAATT        rFH4.3
          TTATATTATGGACTGTTTGTGTAGCAGAAGATTGTAAAGGTCCTCCTCCAAGAGAAAATT        rFH2.7
          TTATATTATGGACTGTTTGTGTAGCAGAAGATTGTAAAGGTCCTCCTCCAAGAGAAAATT        rFH1.8
          TTATATTATGGACTGTTTGTGTAGCAGAAGATTGTAAAGGTCCTCCTCCAAGAGAAAATT        rFH1.0


                    130       140       150       160       170       180
          CAGAAATTCTCTCAGGTTCGTGGTCTGAACAACTATATTCAGAAGGCACTCAGGCAACCT        rFH4.3
          CAGAAATTCTCTCAGGTTCGTGGTCTGAACAACTATATTCAGAAGGCACTCAGGCAACCT        rFH2.7
          CAGAAATTCTCTCAGGTTCGTGGTCTGAACAACTATATTCAGAAGGCACTCAGGCAACCT        rFH1.8
          CAGAAATTCTCTCAGGTTCGTGGTCTGAACAACTATATTCAGAAGGCACTCAGGCAACCT        rFH1.0


                    190       200       210       220       230       240
          ACAAATGCCGCCCTGGATACCGAACACTTGGTACTATTGTAAAAGTATGCAAGAATGGAG        rFH4.3
          ACAAATGCCGCCCTGGATACCGAACACTTGGTACTATTGTAAAAGTATGCAAGAATGGAG        rFH2.7
          ACAAATGCCGCCCTGGATACCGAACACTTGGTACTATTGTAAAAGTATGCAAGAATGGAG        rFH1.8
          ACAAATGCCGCCCTGGATACCGAACACTTGGTACTATTGTAAAAGTATGCAAGAATGGAG        rFH1.0


                                        SCR2a
                    250       260       270       280       290       300
          AATGGGTACCTTCTAACCCATCAAGGATATGTCGGAAAAGGCCATGTGGGCATCCCGGAG        rFH4.3
          AATGGGTACCTTCTAACCCATCAAGGATATGTCGGAAAAGGCCATGTGGGCATCCCGGAG        rFH2.7
          AATGGGTACCTTCTAACCCATCAAGGATATGTCGGAAAAGGCCATGTGGGCATCCCGGAG        rFH1.8
          AATGGGTACCTTCTAACCCATCAAGGATATGTCGGAAAAGGCCATGTGGGCATCCCGGAG        rFH1.0


                    310       320       330       340       350       360
          ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG        rFH4.3
          ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG        rFH2.7
          ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG        rFH1.8
          ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG        rFH1.0
```

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                            SCR2b
        370        380        390        400        410        420
TTGTTTATACATGTGATGAAGGGTACCAACTATTAGGTGAAATTGATTACCGTGAATGTG      rFH4.3
TTGTTTATACATGTGATGAAGGGTACCAACTATTAGGTGAAATTGATTACCGTGAATGTG      rFH2.7
TTGTTTATACATGTGATGAAGGGTACCAACTATTAGGTGAAATTGATTACCGT-------      rFH1.8
TTGTTTATACATGTGATGAAGGGTACCAACTATTAGGTGAAATTGATTACCGTGAATGTG      rFH1.0


                            SCR3
        430        440        450        460        470        480
ATGCAGATGGGTGGACCAATGATATTCCAATATGTGAAGTTGTGAAGTGCTTGCCAGTGA      rFH4.3
ATGCAGATGGGTGGACCAATGATATTCCAATATGTGAAGTTGTGAAGTGCTTGCCAGTGA      rFH2.7
------------------------------------------------------------      rFH1.8
ATGCAGATGGGTGGACCAATGATATTCCAATATGTGAAGTTGTGAAGTGCTTGCCAGTGA      rFH1.0



        490        500        510        520        530        540
CAGAACTGGAGAATGGAAGAATTGTGAGTGGTGCAGCCGAACCAGACCAGGAATATTATT      rFH4.3
CAGAACTGGAGAATGGAAGAATTGTGAGTGGTGCAGCCGAACCAGACCAGGAATATTATT      rFH2.7
------------------------------------------------------------      rFH1.8
CAGAACTGGAGAATGGAAGAATTGTGAGTGGTGCAGCCGAACCAGACCAGGAATATTATT      rFH1.0



        550        560        570        580        590        600
TTGGACAGGTGGTACGCTTTGAATGCAACTCCGGCTTCAAGATTGAAGGACAGAAAGAAA      rFH4.3
TTGGACAGGTGGTACGCTTTGAATGCAACTCCGGCTTCAAGATTGAAGGACAGAAAGAAA      rFH2.7
------------------------------------------------------------      rFH1.8
TTGGACAGGTGGTACGCTTTGAATGCAACTCCGGCTTCAAGATTGAAGGACAGAAAGAAA      rFH1.0


                                                  SCR4
        610        620        630        640        650        660
TGCACTGCTCATAAAATGGCCTCTGGAGCAATGAAAAGCCACAGTGTGTGGAAATTTCTT      rFH4.3
TGCACTGCTCATAAAATGGCCTCTGGAGCAATGAAAAGCCACAGTGTGTG----------      rFH2.7
------------------------------------------------------------      rFH1.8
TGCACTGCTCATAAAATGGCCTCTGGAGCAATGAAAAGCCACAGTGTGTGGAAATTTCTT      rFH1.0



        670        680        690        700        710        720
GCCTGCCACCACGAGTTGAAAATGGAGATGGTATATATCTGAAACCAGTTTACAAGGAGA      rFH4.3
------------------------------------------------------------      rFH2.7
------------------------------------------------------------      rFH1.8
GCCTGCCACCACGAGTTGAAAATGGAGAT-------------------------------      rFH1.0
```

```
                730       740       750       760       770       780
     ATGAAAGATTCCAATATAAATGTAAGCAAGGTTTTGTGTACAAAGAAAGAGGGGATGCTG        rFH4.3
     ------------------------------------------------------------        rFH2.7
     ------------------------------------------------------------        rFH1.8
     ------------------------------------------------------------        rFH1.0


                                              SCR5
                790       800       810       820       830       840
     TCTGCACGGGTTCTGGATGGAATCCTCAGCCTTCCTGTGAAGAAATGACATGTTTGACTC        rFH4.3
     ------------------------------------------------------------        rFH2.7
     ------------------------------------------------------------        rFH1.8
     ------------------------------------------------------------        rFH1.0


                850       860       870       880       890       900
     CATATATTCCAAATGGTATCTACACACCTCACAGGATTAAACACAGAATTGATGATGAAA        rFH4.3
     ------------------------------------------------------------        rFH2.7
     ------------------------------------------------------------        rFH1.8
     ------------------------------------------------------------        rFH1.0


                910       920       930       940       950       960
     TCAGATATGAATGTAAAAATGGCTTCTATCCTGCAACCCGATCACCTGTTTCAAAGTGTA        rFH4.3
     ------------------------------------------------------------        rFH2.7
     ------------------------------------------------------------        rFH1.8
     ------------------------------------------------------------        rFH1.0


                                          SCR6
                970       980       990      1000      1010      1020
     CAATTACTGGCTGGATCCCTGCTCCAAGATGTAGCTTGAAACCTTGTGATTTTCCACAAT        rFH4.3
     ----------------------------------------TTGAAACCTTGTGATTTTCCACAAT        rFH2.7
     ------------------------------------------------------------        rFH1.8
     ------------------------------------------------------------        rFH1.0


               1030      1040      1050      1060      1070      1080
     TCAAACATGGACGTCTGTATTATGAAGAAAGCCGGAGACCCTACTTCCCAGTACCTATAG        rFH4.3
     TCAAACATGGACGTCTGTATTATGAAGAAAGCCGGAGACCCTACTTCCCAGTACCTATAG        rFH2.7
     ------------------------------------------------------------        rFH1.8
     ------------------------------------------------------------        rFH1.0
```

```
          1090      1100      1110      1120      1130      1140
GAAAGGAGTACAGCTATAACTGTGACAACGGGTTTACAACGCCTTCACAGTCATACTGGG    rFH4.3
GAAAGGAGTACAGCTATAACTGTGACAACGGGTTTACAACGCCTTCACAGTCATACTGGG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


                                                    SCR7
          1150      1160      1170      1180      1190      1200
ACTACCTTCGTTGCACAGTAAATGGGTGGGAGCCTGAAGTTCCATGCCTCAGGCAATGTA    rFH4.3
ACTACCTTCGTTGCACAGTAAATGGGTGGGAGCCTGAAGTTCCATGCCTCAGGCAATGTA    rFH2.7
-----------------------------------------------------------     rFH1.8
-----------------------------------------------------------     rFH1.0


          1210      1220      1230      1240      1250      1260
TTTTCCATTATGTGGAATATGGAGAATCTTCATACTGGCAAAGAAGATATATAGAGGGTC    rFH4.3
TTTTCCATTATGTGGAATATGGAGAATCTTCATACTGGCAAAGAAGATATATAGAGGGTC    rFH2.7
-----------------------------------------------------------     rFH1.8
-----------------------------------------------------------     rFH1.0


          1270      1280      1290      1300      1310      1320
AGTCTGCAAAAGTCCAGTGTCACAGTGGCTATAGTCTTCCAAATGGTCAAGATACATATT    rFH4.3
AGTCTGCAAAAGTCCAGTGTCACAGTGGCTATAGTCTTCCAAATGGTCAAGATACATATT    rFH2.7
-----------------------------------------------------------     rFH1.8
-----------------------------------------------------------     rFH1.0


                                                    SCR8
          1330      1340      1350      1360      1370      1380
ATTGTACAGAGAATGGCTGGTCCCCTCCTCCCAAATGCGTCCGTATCAAGACTTGTTCAG    rFH4.3
ATTGTACAGAGAATGGCTGGTCCCCTCCTCCCAAATGCGTCCGTATCAAGACTTGTTCAG    rFH2.7
-----------------------------------------------------------     rFH1.8
-----------------------------------------------------------     rFH1.0


          1390      1400      1410      1420      1430      1440
TATCAGATATAGAAATTGAAAATGGGTTTTTTTCTGAATCTGATTATACATATGCTCTAA    rFH4.3
TATCAGATATAGAAATTGAAAATGGGTTTTTTTCTGAATCTGATTATACATATGCTCTAA    rFH2.7
-----------------------------------------------------------     rFH1.8
-----------------------------------------------------------     rFH1.0
```

```
            1450      1460      1470      1480      1490      1500
ATAGAAAAACACGGTATAGATGTAAACAGGGATATGTAACAAATACCGGAGAAATATCAG    rFH4.3
ATAGAAAAACACGGTATAGATGTAAACAGGGATATGTAACAAATACCGGAGAAATATCAG    rFH2.7
------------------------------------------------------------    rFH1.8
                                                                rFH1.0


                                                         SCR9
            1510      1520      1530      1540      1550      1560
GAATAATTACTTGTCTTCAAGATGGATGGTCACCTCGACCCTCATGCATTAAGTCTTGTG    rFH4.3
GAATAATTACTTGTCTTCAAGATGGATGGTCACCTCGACCCTCATGCATTAAGTCTTGTG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            1570      1580      1590      1600      1610      1620
ATATGCCTGTATTTGAGAATTCTATGACTAAGAATAATAACACATGGTTTAAACTCAATG    rFH4.3
ATATGCCTGTATTTGAGAATTCTATGACTAAGAATAATAACACATGGTTTAAACTCAATG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            1630      1640      1650      1660      1670      1680
ACAAATTAGACTATGAATGTCACATTGGATATGAAAATGAATATAAACATACCAAAGGCT    rFH4.3
ACAAATTAGACTATGAATGTCACATTGGATATGAAAATGAATATAAACATACCAAAGGCT    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


                                                         SCR10
            1690      1700      1710      1720      1730      1740
CTATAACATGTACTTATGATGGATGGTCTAGTACACCCTCCTGTTATGAAAGAGAATGCA    rFH4.3
CTATAACATGTACTTATGATGGATGGTCTAGTACACCCTCCTGTTATGAAAGAGAATGCA    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            1750      1760      1770      1780      1790      1800
GCATTCCCCTGTTACACCAAGACTTAGTTGTTTTTCCCAGAGAAGTAAAATACAAAGTTG    rFH4.3
GCATTCCCCTGTTACACCAAGACTTAGTTGTTTTTCCCAGAGAAGTAAAATACAAAGTTG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
            1810        1820        1830        1840        1850        1860
GAGATTCGTTGAGTTTCTCTTGCCGTTCAGGACACAGAGTTGGAGCAGATTTAGTGCAAT    rFH4.3
GAGATTCGTTGAGTTTCTCTTGCCGTTCAGGACACAGAGTTGGAGCAGATTTAGTGCAAT    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


                                                   SCR11
            1870        1880        1890        1900        1910        1920
GCTACCACTTTGGATGGTCCCCTAATTTCCCAACGTGTGAAGGCCAAGTAAAATCATGTG    rFH4.3
GCTACCACTTTGGATGGTCCCCTAATTTCCCAACGTGTGAAGGCCAAGTAAAATCATGTG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            1930        1940        1950        1960        1970        1980
ACCAACCTCTTGAAATCCCGAATGGGGAAATAAAGGGAACAAAAAAAGTTGAATACAGCC    rFH4.3
ACCAACCTCTTGAAATCCCGAATGGGGAAATAAAGGGAACAAAAAAAGTTGAATACAGCC    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            1990        2000        2010        2020        2030        2040
ATGGTGACGTGGTGGAATATGATTGCAAACCTAGATTTCTACTGAAGGGACCCAATAAAA    rFH4.3
ATGGTGACGTGGTGGAATATGATTGCAAACCTAGATTTCTACTGAAGGGACCCAATAAAA    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


                                                   SCR12
            2050        2060        2070        2080        2090        2100
TCCAGTGTGTTGACGGGAAGTGGACAAGGTTGCCGATATGCGTTGAGTATGAGAGAACAT    rFH4.3
TCCAGTGTGTTGACGGGAAGTGGACAAGGTTGCCGATATGCGTTGAGTATGAGAGAACAT    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            2110        2120        2130        2140        2150        2160
GTGGAGACCTTCCTGAACTTGAGCATGGCTCTGTCAAGTTATCTGTCCCTCCCTACCATC    rFH4.3
GTGGAGACCTTCCTGAACTTGAGCATGGCTCTGTCAAGTTATCTGTCCCTCCCTACCATC    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
        2170      2180      2190      2200      2210      2220
ATGGAGATTCAGTGGAGTTCACTTGTACAGAAACCTTCACAATGATTGGACATGCAGTAG    rFH4.3
ATGGAGATTCAGTGGAGTTCACTTGTACAGAAACCTTCACAATGATTGGACATGCAGTAG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
                                            SCR13
        2230      2240      2250      2260      2270      2280
TTTTCTGCATTAGTGGAAGGTGGACCGAGCTTCCTCAATGTGTTGCAACAGATCAACTGG    rFH4.3
TTTTCTGCATTAGTGGAAGGTGGACCGAGCTTCCTCAATGTGTTGCAACAGATCAACTGG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
        2290      2300      2310      2320      2330      2340
AGAAGTGTAAAGCCCCGAAGTCAACTGGCATAGATGCAATTCATCCAAATAAGAATGAAT    rFH4.3
AGAAGTGTAAAGCCCCGAAGTCAACTGGCATAGATGCAATTCATCCAAATAAGAATGAAT    rFH2.7
------------------------------------------------------------    rFH1.8
                                                                rFH1.0
```

```
        2350      2360      2370      2380      2390      2400
TTAATCATAACTTTAGTGTGAGTTACAGATGTAGACAAAAGCAGGAGTATGAACATTCAA    rFH4.3
TTAATCATAACTTTAGTGTGAGTTACAGATGTAGACAAAAGCAGGAGTATGAACATTCAA    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
                                    SCR14
        2410      2420      2430      2440      2450      2460
TCTGCATCAATGGAAGATGGGATCCTGAACCAAACTGTACAAGCAAAAGATTCTGCCCTC    rFH4.3
TCTGCATCAATGGAAGATGGGATCCTGAACCAAACTGTACAAGCAAAAGATTCTGCCCTC    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
        2470      2480      2490      2500      2510      2520
CTCCCCCGCAGATTCCAAATGCCCAAGTGATTGAAACCACCGTGAAATACTTGGATGGAG    rFH4.3
CTCCCCCGCAGATTCCAAATGCCCAAGTGATTGAAACCACCGTGAAATACTTGGATGGAG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
          2530      2540      2550      2560      2570      2580
AAAAAGTATCTGTTCTTTGCCAAGATGGTTACCTAACTCAGGGCCCAGAAGAAATGGTGT   rFH1.8
AAAAAGTATCTGTTCTTTGCCAAGATGGTTACCTAACTCAGGGCCCAGAAGAAATGGTGT   rFH2.7
------------------------------------------------------------   rFH4.3
------------------------------------------------------------   rFH1.0


                                        SCR15
          2590      2600      2610      2620      2630      2640
GTAAACATGGAAGGTGGCAGTCGTTACCACGCTGCACGGAAAAAATTCCATGTTCCCAGC   rFH4.3
GTAAACATGGAAGGTGGCAGTCGTTACCACGCTGCACGGAAAAAATTCCATGTTCCCAGC   rFH2.7
------------------------------------------------------------   rFH1.8
------------------------------------------------------------   rFH1.0


          2650      2660      2670      2680      2690      2700
CCCCTAAAATTGAACATGGATCTATTAAGTCGCCCAGGTCCTCAGAAGAGAGGAGAGATT   rFH4.3
CCCCTAAAATTGAACATGGATCTATTAAGTCGCCCAGGTCCTCAGAAGAGAGGAGAGATT   rFH2.7
------------------------------------------------------------   rFH1.8
------------------------------------------------------------   rFH1.0


          2710      2720      2730      2740      2750      2760
TAATTGAGTCCAGCAGTTATGAACACGGAACTACATTCAGCTATTGCTGTAGAGATGGAT   rFH4.3
TAATTGAGTCCAGCAGTTATGAACACGGAACTACATTCAGCTATTGCTGTAGAGATGGAT   rFH2.7
------------------------------------------------------------   rFH1.8
------------------------------------------------------------   rFH1.0


          2770      2780      2790      2800      2810      2820
TCAAGATATCTGAAGAAAATAGGGTAACCTGCAACATGGGAAAATGGAGCTCTCTGCCTC   rFH4.3
TCAAGATATCTGAAGAAAATAGGGTAACCTGCAACATGGGAAAATGGAGCTCTCTGCCTC   rFH2.7
------------------------------------------------------------   rFH1.8
------------------------------------------------------------   rFH1.0


       SCR16
          2830      2840      2850      2860      2870      2880
GTTGTGTTGGAATACCTTGTGGACCCCCACCTTCAATTCCTCTTGGTATTGTTTCTCATG   rFH4.3
GTTGTGTTGGAATACCTTGTGGACCCCCACCTTCAATTCCTCTTGGTATTGTTTCTCATG   rFH2.7
------------------------------------------------------------   rFH1.8
------------------------------------------------------------   rFH1.0
```

```
              2890      2900      2910      2920      2930      2940
AACTAGAAAGTTACCAATATGGAGAGGAGGTTACATACAATTGTTCTGAAGGCTTTGGAA      rFH4.3
AACTAGAAAGTTACCAATATGGAGAGGAGGTTACATACAATTGTTCTGAAGGCTTTGGAA      rFH2.7
------------------------------------------------------------      rFH1.8
------------------------------------------------------------      rFH1.0


              2950      2960      2970      2980      2990      3000
TTGATGGACCAGCATTTATTAAATGTGTAGGAGGACAGTGGTCTGAACCTCCCAAATGCA      rFH4.3
TTGATGGACCAGCATTTATTAAATGTGTAGGAGGACAGTGGTCTGAACCTCCCAAATGCA      rFH2.7
------------------------------------------------------------      rFH1.8
------------------------------------------------------------      rFH1.0


    SCR17
              3010      3020      3030      3040      3050      3060
TAAAAACTGATTGTGACAACTTGCCCACATTTGAAATTGCCAAACCGACAGAAAAGAAAA      rFH4.3
TAAAAACTGATTGTGACAACTTGCCCACATTTGAAATTGCCAAACCGACAGAAAAGAAAA      rFH2.7
------------------------------------------------------------      rFH1.8
------------------------------------------------------------      rFH1.0


              3070      3080      3090      3100      3110      3120
AAAAATCATACAGGTCAGGAGAACAAGTGACATTCAGATGTCCACCTCCGTATCGAATGG      rFH4.3
------------------------------------------------------------      rFH2.7
----------------------------------------------TATCGAATGG      rFH1.8
------------------------------------------------------------      rFH1.0


              3130      3140      3150      3160      3170      3180
ATGGCTCTGACATTGTCACATGTGTTAATACGAAGTGGATTGGACAGCCGGTATGCAAAG      rFH4.3
------------------------------------------------------------      rFH2.7
ATGGCTCTGACATTGTCACATGTGTTAATACGAAGTGGATTGGACAGCCGGTATGCAAAG      rFH1.8
------------------------------------------------------------      rFH1.0


    SCR18
              3190      3200      3210      3220      3223      3240
ATAATTCCTGTGTGAATCCACCACATGTGCCAAATGCTACTATACTAACAAGGCACAAGA      rFH4.3
------------------------------------------------------------      rFH2.7
ATAATTCCTGTGTGAATCCACCACATGTGCCAAATGCTACTATACTAACAAGGCACAAGA      rFH1.8
------------------------------------------------------------      rFH1.0
```

```
          3250      3260      3270      3280      3290      3300
CTAAATATCCATCTGGTGACAAAGTACGTTATGACTGTAATAAACCTTTTGAATTATTTG      rFH4.3
-----------------------------------------------------------      rFH2.7
CTAAATATCCATCTGGTGACAAAGTACGTTATGACTGTAATAAACCTTTTGAATTATTTG      rFH1.8
-----------------------------------------------------------      rFH1.0


          3310      3320      3330      3340      3350      3360
GGGAAGTGGAAGTGATGTGCCAAAACGGGATTTGGACAGAACCACCGAAATGCAAAGATT      rFH4.3
-----------------------------------------------------------      rFH2.7
GGGAAGTGGAAGTGATGTGCCAAAACGGGATTTGGACAGAACCACCGAAATGCAAAGATT      rFH1.8
-----------------------------------------------------------      rFH1.0


     SCR19
          3370      3380      3390      3400      3410      3420
CAACAGGGAAATGTGGGCCTCCTCCACCTATTGACAATGGAGACATCACCTCCTTGTCAT      rFH4.3
-----------------------------------------------------------      rFH2.7
CAACAGGGAAATGTGGGCCTCCTCCACCTATTGACAATGGAGACATCACCTCCTTGTCAT      rFH1.8
-----------------------------------------------------------      rFH1.0


          3430      3440      3450      3460      3470      3480
TACCAGTATATGCACCATTATCATCAGTTGAATATCAATGCCAGAACTATTATCTACTTA      rFH4.3
-----------------------------------------------------------      rFH2.7
TACCAGTATATGCACCATTATCATCAGTTGAATATCAATGCCAGAACTATTATCTACTTA      rFH1.8
-----------------------------------------------------------      rFH1.0


          3490      3500      3510      3520      3530      3540
AGGGAAATAAGATAGTAACATGTAGAAATGGAAAGTGGTCTCAGCCACCAACCTGCTTAC      rFH4.3
-----------------------------------------------------------      rFH2.7
AGGGAAATAAGATAGTAACATGTAGAAATGGAAAGTGGTCTCAGCCACCAACCTGCTTAC      rFH1.8
-----------------------------------------------------------      rFH1.0


     SCR20
          3550      3560      3570      3580      3590      3600
ATGCATGTGTGATACCAGAAGATATTATGGAAAAACATAATATAGTTCTCAGATGGAGGG      rFH4.3
-----------------------------------------------------------      rFH2.7
ATGCATGTGTGATACCAGAAGATATTATGGAAAAACATAATATAGTTCTCAGATGGAGGG      rFH1.8
-----------------------------------------------------------      rFH1.0
```

```
          3610      3620      3630      3640      3650      3660
AAAATGCAAAGATTTATTCCCAATCAGGGGAGAATATTGAATTCATGTGTAAACCTGGAT   rFH4.3
-----------------------------------------------------------   rFH2.7
AAAATGCAAAGATTTATTCCCAATCAGGGGAGAATATTGAATTCATGTGTAAACCTGGAT   rFH1.8
----------------------------------------------------GGAT      rFH1.0


          3670      3680      3690      3700      3710      3720
ATAGAAAATTCAGAGGATCACCTCCGTTTCGTACAAAGTGCATTGAGGGTCACATCAATT   rFH4.3
-----------------------------------------------------------   rFH2.7
ATAGAAAATTCAGAGGATCACCTCCGTTTCGTACAAAGTGCATTGAGGGTCACATCAATT   rFH1.8
ATAGAAAATTCAGAGGATCACCTCCGTTTCGTACAAAGTGCATTGAGGGTCACATCAATT   rFH1.0


          3730      3740      3750      3760      3770      3780
ATCCCACTTGTGTATAAaatcgctatacaattattagtaaaccttatggatgagaaatgc   rFH4.3
-----------------------------------------------------------   rFH2.7
ATCCCACTTGTGTATAAaatcgctatacaattattagtaaaccttatggatgagaaatgc   rFH1.8
ATCCCACTTGTGTATAAaatcgctatacaattattagtaaaccttatggatgacactttg   rFH1.0


          3790      3800      3810      3820      3830      3840
acatgtatattactaatacagtttgaatttacatttaaatattgtttagctcatttcctc   rFH4.3
-----------------------------------------------------------   rFH2.7
acatgtatattactaatacagtttgaatttacatttaaatattgtttagctcatttcctc   rFH1.8
tttagaaatgcacatgtatattactaatacagtttgaatttacatttgaaaaa-------   rFH1.0


          3850      3860      3870      3880      3890      3900
taataagtatataaacttttttttatatggtggttaatcagtaactttacagactgttgcc   rFH4.3
------------------------------------------------------------   rFH2.7
taataagtatataaacttttttttatatggtggttaatcagtaactttacagactgttgcc   rFH1.8
-----------------------------------------------------------   rFH1.0
```

```
          3910      3920      3930      3940      3950      3960
acaaagcaagaacattacattcaaaactcctaatccaaatatgatatgtccaaggacaaa    rFH4.3
------------------------------------------------------------    rFH2.7
acaaagcaagaacattacattcaaaactcctaatccaaatatgatatgtccaaggacaaa    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
          3970      3980      3990      4000      4010      4020
ctatgtctaagcaagaaaataaatgttagttcttcaatgtctgttttttattcaggacctt    rFH4.3
------------------------------------------------------------    rFH2.7
ctatgtctaagcaagaaaataaatgttagttcttcaatgtctgttttttattcaggacctt    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
          4030      4040      4050      4060      4070      4080
tcagatttttcttggatacctttttgttaggttctgattcacagtgagtggaagacacactg    rFH4.3
------------------------------------------------------------    rFH2.7
tcagatttttcttggatacctttttgttaggttctgattcacagtgagtggaagacacactg    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
          4090      4100      4110      4120      4130      4140
actctgacttcaaattagtattacttgcaatacattaacaaccaaactatcataatatca    rFH4.3
------------------------------------------------------------    rFH2.7
actctgacttcaaattagtattacttgcaatacattaacaaccaaactatcataatatca    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
          4150      4160      4170      4180      4190      4200
caaatgtatacagctaattactgtgtcctacctttgtatcaataaagaaatctaagaaag    rFH4.3
------------------------------------------------------------    rFH2.7
caaatgtatacagctaattactgtgtcctacctttgtatcaataaagaaatctaagaaag    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
          4210      4220      4230
ttcttgcttaaaaaaaaaaaaaaaaaaaaa                                  rFH4.3
------------------------------                                  rFH2.7
ttcttgcttaaaaaaaaaaaaaaaaaaaaa                                  rFH1.8
------------------------------                                  rFH1.0
```